WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Monday, September 11, 2006

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR	
☐	L4	L3 and psi	3
☐	L3	MLV same gag same pol same pol near GaLV	3
☐	L2	MLV same gag same pol same chimer$ near pol near GaLV	0
☐	L1	MLV or (Moloney adj Murine adj Leukemia)	10929

END OF SEARCH HISTORY

```
     (FILE 'HOME' ENTERED AT 11:53:49 ON 11 SEP 2006)

     FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 11:54:18 ON
     11 SEP 2006
L1             47 MLV(S)GAG(S)POL(S)ENV
L2             97 GALV(S)ENV
L3              3 L1 AND L2
L4           1118 GIBBON APE LEUKEMIA VIRUS
L5              2 DUP REM L3 (1 DUPLICATE REMOVED)
```

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:         July 22, 2006, 03:10:06 ; Search time 199 Seconds
                                           (without alignments)
                                           1553.157 Million cell updates/sec

Title:          US-10-677-558-3
Perfect score:  3630
Sequence:       1 MARSTLSKPPQDKINPWKPL..........VQALVLTQQYHQLKPIEYEP 676

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_8:*
                1:  geneseqp1980s:*
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                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
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                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
                9:  geneseqp2005s:*
                10:  geneseqp2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                        SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB  ID                         Description
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     1  3490.5   96.2    686  7  ADG86764                   Adg86764 Glycoprot
     2    3472   95.6    685  4  AAB19876                   Aab19876 Gibbon le
     3  3405.5   93.8    685  3  AAY93366                   Aay93366 Amino aci
     4  3373.5   92.9    667  2  AAW80289                   Aaw80289 Truncated
     5  3373.5   92.9    667  3  AAY54268                   Aay54268 Amino aci
     6  3373.5   92.9    667  3  AAY93369                   Aay93369 Amino aci
     7    3355   92.4    666  4  AAB19880                   Aab19880 Gibbon le
     8    3260   89.8    956  9  AEA36460                   Aea36460 ScFV-GaLV
     9    2083   57.4    420  7  ADH76471                   Adh76471 Chimeric
    10  1660.5   45.7    675  9  AED10971                   Aed10971 FV envelo
    11  1655.5   45.6    676  5  ABB09158                   Abb09158 Friend mu
    12  1654.5   45.6    673  2  AAW81573                   Aaw81573 Mus dunni
    13  1653.5   45.6    675  5  ABB09155                   Abb09155 Murine le
    14  1644.5   45.3    672  5  ABB09154                   Abb09154 Murine le
    15  1642.5   45.2    675  5  ABB09156                   Abb09156 Murine le
    16  1637.5   45.1    672  5  ABB09153                   Abb09153 Murine le
    17    1636   45.1    654  2  AAY26900                   Aay26900 Amphotrop
    18  1635.5   45.1    675  5  ABB09157                    Abb09157 Murine le
    19    1635   45.0    654  2  AAY26905                    Aay26905 Amphotrop
    20    1634   45.0    654  3  AAY54270                    Aay54270 Envelope
    21    1634   45.0    666  3  AAY93370                    Aay93370 Amino aci
    22    1633   45.0    654  4  AAB19884                    Aab19884 Murine le
    23  1632.5   45.0    647  2  AAY26907                    Aay26907 Amphotrop
    24    1632   45.0    654  2  AAY26899                    Aay26899 Amphotrop
    25    1628   44.8    654  2  AAY26901                    Aay26901 Amphotrop
    26  1625.5   44.8    668  5  ABB09159                    Abb09159 Friend mu
    27    1624   44.7    642  2  AAY26902                    Aay26902 Amphotrop
    28  1623.5   44.7    665  2  AAY26908                    Aay26908 Amphotrop
    29    1623   44.7    646  2  AAY26903                    Aay26903 Amphotrop
    30    1623   44.7    654  2  AAY26898                    Aay26898 Amphotrop
    31    1622   44.7    654  4  AAB19886                    Aab19886 Murine le
    32    1621   44.7    654  4  AAB19882                    Aab19882 Murine le
    33    1618   44.6    654  8  ADE84719                    Ade84719 Murine le
    34  1615.5   44.5    665  3  AAB10045                    Aab10045 MMLV env
    35  1615.5   44.5    665  3  AAY54267                    Aay54267 Amino aci
    36  1615.5   44.5    665  9  AED10939                    Aed10939 MoMLV env
    37  1615.5   44.5    665  10  AEF69292                    Aef69292 Moloney m
    38  1614.5   44.5    653  4  AAB19885                    Aab19885 Murine le
    39  1613.5   44.4    653  4  AAB19874                    Aab19874 Amphotrop
    40  1613.5   44.4    665  2  AAY17948                    Aay17948 MoMLV env
    41  1611.5   44.4    649  2  AAY26904                    Aay26904 Amphotrop
    42    1607   44.3    640  2  AAY26911                    Aay26911 Amphotrop
    43    1606   44.2    640  2  AAY26906                    Aay26906 Amphotrop
    44  1605.5   44.2    641  4  AAB19877                    Aab19877 Murine le
    45  1603.5   44.2    653  4  AAB19887                    Aab19887 Murine le


                                  ALIGNMENTS


RESULT 1
ADG86764
ID   ADG86764 standard; protein; 686 AA.
XX
AC   ADG86764;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Glycoprotein related amino acid #SEQ ID 4.
XX
KW   Cytostatic; gene therapy; glycoprotein; murine leukemia virus A; MLV-A;
KW   feline endogenous virus RD 114; viral; vector; haematopoietic;
KW   lymphohematopoietic; disease; tumour; chimeric.
XX
OS   Synthetic.
XX
PN   WO2003091442-A1.
XX
PD   06-NOV-2003.
XX
PF   25-APR-2003; 2003WO-IB001597.
XX
PR   26-APR-2002; 2002US-0375654P.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (CLAY-) INST CLAYTON RECH.
XX
PI   Trono D,  Cosset F,  Sandrin V,  Boson B,  Negre D;
XX
DR   WPI; 2003-877334/81.
DR   N-PSDB; ADG86763.
XX
PT   New chimeric glycoprotein comprising a cytoplasmic tail domain derived
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```
Title:           US-10-677-558-5
Perfect score:   11394
Sequence:        1 gaattcataccagatcaccg..........cgaggccctttcgtcttcaa 11394

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
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                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                       SUMMARIES
                 %
Result           Query
   No.   Score   Match Length DB  ID                         Description
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     1   11394   100.0  11394  2  DD165435                   DD165435 CHIMERIC
     2   11394   100.0  11394  2  AX768032                   AX768032 Sequence
     3 11322.4    99.4  11364  2  DD165441                   DD165441 CHIMERIC
     4 11322.4    99.4  11364  2  AX768038                   AX768038 Sequence
     5  9717.6    85.3  11328  8  AF010170                   AF010170 Plasmid p
     6    8889    78.0   8889  2  DD165434                   DD165434 CHIMERIC
     7    8889    78.0   8889  2  AX768031                   AX768031 Sequence
c    8  6387.6    56.1   8202  2  I81373                     I81373 Sequence 13
     9  6380.8    56.0   8332  2  BD082109                   BD082109 Non-immun
    10  6380.8    56.0   8332  2  AR229463                   AR229463 Sequence
    11  6380.8    56.0   8332  2  AR229591                   AR229591 Sequence
    12  6380.8    56.0   8332  2  AR341302                   AR341302 Sequence
    13  6380.8    56.0   8332  2  AR595816                   AR595816 Sequence
    14  6380.8    56.0   8332  10  MLMCG                      J02255 Moloney mur
    15  6185.8    54.3   8332  2  AR224436                   AR224436 Sequence
    16  6185.8    54.3   8332  2  AR352468                   AR352468 Sequence
    17  6185.8    54.3   8332  10  AF033811                   AF033811 Moloney m
    18  6161.4    54.1   8332  10  AF462057                   AF462057 Moloney m
    19  5898.6    51.8   8217  10  AF411814                   AF411814 Amphotrop
    20  5885.4    51.7   8231  10  CASBREML                   X57540 CAS-BR-E mu
    21  5530.4    48.5   8358  10  D88386                     D88386 Friend muri
    22  5529.8    48.5   8359  10  REFMLVCG                   X02794 Friend muri
    23  5516.6   48.4   8323  2  A42090                       A42090 Sequence 2
    24  5516.6   48.4   8323  2  AR074024                     AR074024 Sequence
    25  5516.6   48.4   8323  2  AR177655                     AR177655 Sequence
    26  5516.6   48.4   8323  2  I50881                       I50881 Sequence 8
    27  5516.6   48.4   8323  2  AR777921                     AR777921 Sequence
    28  5516.6   48.4   8323  10  REFMLVCGD                    Z11128 Friend muri
    29  5494.6   48.2   8282  10  RMU94692                     U94692 Rauscher mu
    30  5453.8   47.9   8282  10  MULV13893                    Y13893 Murine leuk
    31  5452.2   47.9   8282  10  MLFCG                        M93134 Friend muri
    32  5445.2   47.8   8256  10  AF019230                     AF019230 Murine le
    33  5417.6   47.5   8319  10  AB187565                     AB187565 Murine le
    34  5320.2   46.7   8259  10  AB187566                     AB187566 Murine le
    35    5238   46.0   7616  2  A60206                       A60206 Sequence 2
    36    5238   46.0   7616  2  AR122282                     AR122282 Sequence
c   37  5124.8   45.0  10367  2  AR074025                     AR074025 Sequence
c   38  5124.8   45.0  10367  2  I50882                       I50882 Sequence 9
    39  4946.4   43.4   7308  2  A60207                       A60207 Sequence 3
    40  4946.4   43.4   7308  2  AR122283                     AR122283 Sequence
    41  4941.6   43.4   7308  2  A60208                       A60208 Sequence 4
    42  4941.6   43.4   7308  2  AR122284                     AR122284 Sequence
    43  4835.6   42.4   5178  2  BD001900                     BD001900 Method fo
    44  4815.4   42.3   8892  10  MLU43202                     U43202 RFP proviru
    45  4791.2   42.1   8889  2  A47081                       A47081 Sequence 1
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Title:          US-10-677-558-5
Perfect score:  11394
Sequence:       1 gaattcataccagatcaccg..........cgaggccctttcgtcttcaa 11394

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_8:*
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                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB  ID                          Description
 -----------------------------------------------------------------------------

     1 11376.4   99.8  11394  10  ADH76473                    Adh76473 Chimeric
     2 11314.4   99.3  11364  10  ADH76479                    Adh76479 Chimeric
     3  8882.6   78.0   8889  10  ADH76472                    Adh76472 Chimeric
 c   4    6386   56.0   8202  2  AAT09280                    Aat09280 Novel AMP
     5  6380.8   56.0   8332  2  AAV05061                    Aav05061 Moloney m
     6  6380.8   56.0   8332  2  AAV19551                    Aav19551 Retrovira
     7  6380.8   56.0   8332  2  AAV15346                    Aav15346 Retroviru
     8  6380.8   56.0   8332  2  AAV42715                    Aav42715 Moloney m
     9  6380.8   56.0   8332  2  AAX28143                    Aax28143 Retrovira
    10  6380.8   56.0   8332  3  AAZ45539                    Aaz45539 Complete
    11  6380.8   56.0   8332  3  AAZ90064                    Aaz90064 Moloney m
    12  6380.8   56.0   8332  6  ABK33877                    Abk33877 MoMLVgag/
    13  6380.8   56.0   8332  8  ABS57818                    Abs57818 MoMLV ret
    14  6380.8   56.0   8332  13  ADU47537                    Adu47537 pKT-1 pla
    15  6377.6   56.0   8332  2  AAT08452                    Aat08452 MoMLV gag
    16  6377.6   56.0   8332  2  AAT07374                    Aat07374 MoMLV gag
    17  6353.6   55.8   8330  2  AAX77178                    Aax77178 MoMLV gen
    18  6185.8   54.3   8332  3  AAA40297                    Aaa40297 MMLV gag,
    19  6185.8   54.3   8332  15  AEF69289                    Aef69289 Moloney m
    20  5689.6   49.9  12135  2  AAT60555                    Aat60555 Plasmid p
    21  5516.6   48.4   8323  2  AAQ81042                    Aaq81042 Friend mu
    22  5516.6   48.4   8323  2  AAT80058                    Aat80058 LTR clone
```

```
     23  5516.6    48.4    8323   2  AAZ07063                          Aaz07063 Friend ec
     24    5491    48.2    8323   2  AAQ58700                          Aaq58700 LTR clone
     25    5238    46.0    7616   2  AAT90688                          Aat90688 Plasmid C
c    26  5124.8    45.0   10367   2  AAT80057                          Aat80057 Sequence
c    27  5124.8    45.0   10367   2  AAZ07067                          Aaz07067 Glycopept
c    28  5076.8    44.6   10367   2  AAQ58701                          Aaq58701 pLRB332.
     29  4950.6    43.4   36538   2  AAT60558                          Aat60558 Recombina
     30  4946.4    43.4    7308   2  AAT90693                          Aat90693 Plasmid h
     31  4941.6    43.4    7308   2  AAT90694                          Aat90694 Plasmid h
     32  4835.6    42.4    5178   3  AAA15660                          Aaa15660 Gibbon le
     33  4820.2    42.3    8892   2  AAQ94266                          Aaq94266 Osteoindu
     34  4538.4    39.8    8278   4  AAC89138                          Aac89138 Canine re
     35  3526.8    31.0   11228  10   ACH00964                          Ach00964 Pro 542 a
     36  3486.2    30.6    6312   2  AAT90691                          Aat90691 Plasmid F
     37  3470.8    30.5    8535   2  AAQ73731                          Aaq73731 GaLV SEAT
     38  3407.8    29.9    8088   3  AAZ45540                          Aaz45540 Complete
     39  3281.4    28.8    3612   8  ABS57820                          Abs57820 MoMLV ret
     40  3281.2    28.8    6283   4  AAF83147                          Aaf83147 Complete
     41  3271.6    28.7    3643   3  AAA87841                          Aaa87841 MLV rever
     42    3097    27.2    6145   2  AAV83182                          Aav83182 Intermedi
     43    3097    27.2    6145   5  AAF85611                          Aaf85611 M-MuLV-ba
     44  3000.4    26.3    7352   6  ADE82654                          Ade82654 Plasmid v
     45  2999.8    26.3    9009  10   ACH00961                          Ach00961 Bovine al
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```
GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July 23, 2006, 16:49:38 ; Search time 4859 Seconds
                                           (without alignments)
                                           12754.953 Million cell updates/sec

Title:          US-10-677-558-4
Perfect score:  8889
Sequence:       1 tttgaaagaccccacccgta..........gtcagcgggggtctttcatt 8889

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_8:*
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                3:  geneseqn2000s:*
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                5:  geneseqn2001bs:*
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                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB  ID                    Description
-------------------------------------------------------------------------------
     1  8882.6   99.9   8889  10  ADH76472               Adh76472 Chimeric
     2  8871.4   99.8  11394  10  ADH76473               Adh76473 Chimeric
     3    8811   99.1  11364  10  ADH76479               Adh76479 Chimeric
 c   4    6386   71.8   8202  2  AAT09280              Aat09280 Novel AMP
     5  6380.8   71.8   8332  2  AAV05061              Aav05061 Moloney m
     6  6380.8   71.8   8332  2  AAV19551              Aav19551 Retrovira
     7  6380.8   71.8   8332  2  AAV15346              Aav15346 Retroviru
     8  6380.8   71.8   8332  2  AAV42715              Aav42715 Moloney m
     9  6380.8   71.8   8332  2  AAX28143              Aax28143 Retrovira
    10  6380.8   71.8   8332  3  AAZ45539              Aaz45539 Complete
    11  6380.8   71.8   8332  3  AAZ90064              Aaz90064 Moloney m
    12  6380.8   71.8   8332  6  ABK33877              Abk33877 MoMLVgag/
    13  6380.8   71.8   8332  8  ABS57818                      Abs57818 MoMLV ret
    14  6380.8   71.8   8332  13  ADU47537                      Adu47537 pKT-1 pla
    15  6377.6   71.7   8332  2  AAT08452                      Aat08452 MoMLV gag
    16  6377.6   71.7   8332  2  AAT07374                      Aat07374 MoMLV gag
    17  6353.6   71.5   8330  2  AAX77178                      Aax77178 MoMLV gen
    18  6117.2   68.8   8332  3  AAA40297                      Aaa40297 MMLV gag,
    19  6117.2   68.8   8332  15  AEF69289                      Aef69289 Moloney m
    20  5516.6   62.1   8323  2  AAQ81042                      Aaq81042 Friend mu
    21  5516.6   62.1   8323  2  AAT80058                      Aat80058 LTR clone
    22  5516.6   62.1   8323  2  AAZ07063                      Aaz07063 Friend ec
    23    5491   61.8   8323  2  AAQ58700                      Aaq58700 LTR clone
    24    5238   58.9   7616  2  AAT90688                      Aat90688 Plasmid C
c   25  5124.8   57.7  10367  2  AAT80057                      Aat80057 Sequence
c   26  5124.8   57.7  10367  2  AAZ07067                      Aaz07067 Glycopept
c   27  5076.8   57.1  10367  2  AAQ58701                      Aaq58701 pLRB332.
    28  4950.6   55.7  12135  2  AAT60555                      Aat60555 Plasmid p
    29  4950.6   55.7  36538  2  AAT60558                      Aat60558 Recombina
    30  4946.4   55.6   7308  2  AAT90693                      Aat90693 Plasmid h
    31  4941.6   55.6   7308  2  AAT90694                      Aat90694 Plasmid h
    32  4835.6   54.4   5178  3  AAA15660                      Aaa15660 Gibbon le
    33  4820.2   54.2   8892  2  AAQ94266                      Aaq94266 Osteoindu
    34  4538.4   51.1   8278  4  AAC89138                      Aac89138 Canine re
    35  3470.8   39.0   8535  2  AAQ73731                      Aaq73731 GaLV SEAT
    36  3407.8   38.3   8088  3  AAZ45540                      Aaz45540 Complete
    37  3281.4   36.9   3612  8  ABS57820                      Abs57820 MoMLV ret
    38  3271.6   36.8   3643  3  AAA87841                      Aaa87841 MLV rever
    39  2573.4   29.0   8440  2  AAT13265                      Aat13265 FeLV F6A
    40  2101.4   23.6   6312  2  AAT90691                      Aat90691 Plasmid F
    41    2088   23.5   2336  10  ADL18730                      Adl18730 MMLV reve
    42  1976.8   22.2   8388  2  AAQ78191                      Aaq78191 Vector M4
    43  1928.4   21.7   2058  10  ADG86763                      Adg86763 Glycoprot
    44  1928.2   21.7   6180  10  ADH76474                      Adh76474 Chimeric
    45  1910.8   21.5   2055  4  AAA89076                      Aaa89076 GALV enve
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```
GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July 23, 2006, 16:49:24 ; Search time 47811 Seconds
                                           (without alignments)
                                           11889.076 Million cell updates/sec

Title:          US-10-677-558-4
Perfect score:  8889
Sequence:       1 tttgaaagaccccacccgta..........gtcagcgggggtctttcatt 8889

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
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Result          Query
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     9  6380.8   71.8   8332  2  BD082109                  BD082109 Non-immun
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DEFINITION  Plasmid pAMS with hybrid amphotropic/Moloney murine leukemia virus,
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ACCESSION   AF010170
VERSION     AF010170.1  GI:2281586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 11328)
  AUTHORS   Miller,A.D. and Buttimore,C.
  TITLE     Redesign of retrovirus packaging cell lines to avoid recombination
            leading to helper virus production
  JOURNAL   Mol. Cell. Biol. 6 (8), 2895-2902 (1986)
   PUBMED   3785217
REFERENCE   2  (bases 1 to 11328)
  AUTHORS   Miller,A.D.
  TITLE     Hybrid Amphotropic/Moloney Murine Leukemia Virus
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 11328)
  AUTHORS   Miller,A.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1997) Molecular Medicine, Fred Hutchinson Cancer
            Research Center, 1100 Fairview Ave N, Seattle, WA 98109, USA
COMMENT     The retrovirus contained in this plasmid is a reference retrovirus
            for FDA validation of retrovirus vectors used for human gene
            therapy. NIH 3T3 mouse cells producing the virus - ATCC VR-1448.
            Virus preparations - ATCC VR-1450. Related GenBank Accession
            Numbers J02255, M33469, U51729, U87552, AF003736, J01749.
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ORIGIN

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Qy         2221 AGGACCCAGGGCAAGAAACTAATGTGTCTATGTCTTTCATTTGGCAGTCTGCCCCAGACA 2280
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Db         2365 AGGACCCAGGGCAAGAAACTAATGTGTCTATGTCTTTCATTTGGCAGTCTGCCCCAGACA 2424

Qy         2281 TTGGGAGAAAGTTAGAGAGGTTAGAAGATTTAAAAAACAAGACGCTTGGAGATTTGGTTA 2340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2425 TTGGGAGAAAGTTAGAGAGGTTAGAAGATTTAAAAAACAAGACGCTTGGAGATTTGGTTA 2484

Qy         2341 GAGAGGCAGAAAAGATCTTTAATAAACGAGAAACCCCGGAAGAAAGAGAGGAACGTATCA 2400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2485 GAGAGGCAGAAAAGATCTTTAATAAACGAGAAACCCCGGAAGAAAGAGAGGAACGTATCA 2544

Qy         2401 GGAGAGAAACAGAGGAAAAAGAAGAACGCCGTAGGACAGAGGATGAGCAGAAAGAGAAAG 2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2545 GGAGAGAAACAGAGGAAAAAGAAGAACGCCGTAGGACAGAGGATGAGCAGAAAGAGAAAG 2604

Qy         2461 AAAGAGATCGTAGGAGACATAGAGAGATGAGCAAGCTATTGGCCACTGTCGTTAGTGGAC 2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2605 AAAGAGATCGTAGGAGACATAGAGAGATGAGCAAGCTATTGGCCACTGTCGTTAGTGGAC 2664

Qy         2521 AGAAACAGGATAGACAGGGAGGAGAACGAAGGAGGTCCCAACTCGATCGCGACCAGTGTG 2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2665 AGAAACAGGATAGACAGGGAGGAGAACGAAGGAGGTCCCAACTCGATCGCGACCAGTGTG 2724

Qy         2581 CCTACTGCAAAGAAAAGGGGCACTGGGCTAAAGATTGTCCCAAGAAACCACGAGGACCTC 2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2725 CCTACTGCAAAGAAAAGGGGCACTGGGCTAAAGATTGTCCCAAGAAACCACGAGGACCTC 2784

Qy         2641 GGGGACCAAGACCCCAGACCTCCCTCCTGACCCTAGATGACTAGGGAGGTCAGGGTCAGG 2700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2785 GGGGACCAAGACCCCAGACCTCCCTCCTGACCCTAGATGACTAGGGAGGTCAGGGTCAGG 2844

Qy         2701 AGCCCCCCCCTGAACCCAGGATAACCCTCAAAGTCGGGGGGCAACCCGTCACCTTCCTGG 2760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2845 AGCCCCCCCCTGAACCCAGGATAACCCTCAAAGTCGGGGGGCAACCCGTCACCTTCCTGG 2904

Qy         2761 TAGATACTGGGGCCCAACACTCCGTGCTGACCCAAAATCCTGGACCCCTAAGTGATAAGT 2820
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2905 TAGATACTGGGGCCCAACACTCCGTGCTGACCCAAAATCCTGGACCCCTAAGTGATAAGT 2964

Qy         2821 CTGCCTGGGTCCAAGGGGCTACTGGAGGAAAGCGGTATCGCTGGACCACGGATCGCAAAG 2880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2965 CTGCCTGGGTCCAAGGGGCTACTGGAGGAAAGCGGTATCGCTGGACCACGGATCGCAAAG 3024

Qy         2881 TACATCTAGCTACCGGTAAGGTCACCCACTCTTTCCTCCATGTACCAGACTGTCCCTATC 2940
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3025 TACATCTAGCTACCGGTAAGGTCACCCACTCTTTCCTCCATGTACCAGACTGTCCCTATC 3084

Qy         2941 CTCTGTTAGGAAGAGATTTGCTGACTAAACTAAAAGCCCAAATCCACTTTGAGGGATCAG 3000
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3085 CTCTGTTAGGAAGAGATTTGCTGACTAAACTAAAAGCCCAAATCCACTTTGAGGGATCAG 3144

Qy          3001 GAGCTCAGGTTATGGACCAATGGGGCAGCCCCTGCAAGTGTTGACCCTAAATATAGAAG 3060
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3145 GAGCTCAGGTTATGGACCAATGGGGCAGCCCCTGCAAGTGTTGACCCTAAATATAGAAG 3204

Qy          3061 ATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGC 3120
                 ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3205 ATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGC 3264

Qy          3121 TGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAG 3180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3265 TGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAG 3324

Qy          3181 CTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCA 3240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3325 CTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCA 3384

Qy          3241 TGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAA 3300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3385 TGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAA 3444

Qy          3301 TACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGA 3360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3445 TACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGA 3504

Qy          3361 CTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGACATCC 3420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3505 CTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGACATCC 3564

Qy          3421 ACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGT 3480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3565 ACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGT 3624

Qy          3481 ACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGC 3540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3625 ACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGC 3684

Qy          3541 CTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGA 3600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3685 CTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGA 3744

Qy          3601 CCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTGATGAGGCACTGCACAGAG 3660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3745 CCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTGATGAGGCACTGCACAGAG 3804

Qy          3661 ACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACT 3720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3805 ACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACT 3864

Qy          3721 TACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAA 3780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3865 TACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAA 3924

Qy          3781 CCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGG 3840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3925 CCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGG 3984

Qy          3841 TCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAG 3900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3985 TCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAG 4044

Qy          3901 AGACTGTGATGGGGCAGCCTACTCCGAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGA 3960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4045 AGACTGTGATGGGGCAGCCTACTCCGAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGA 4104
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Qy       3961 CGGCAGGCTTCTGTCGCCTCTGGATCCCTGGGTTTGCAGAAATGGCAGCCCCCTTGTACC 4020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4105 CGGCAGGCTTCTGTCGCCTCTGGATCCCTGGGTTTGCAGAAATGGCAGCCCCCTTGTACC 4164

Qy       4021 CTCTCACCAAAACGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAG 4080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4165 CTCTCACCAAAACGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAG 4224

Qy       4081 AAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCT 4140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4225 AAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCT 4284

Qy       4141 TTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGCGTCCTAACGCAAAAGCTGG 4200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4285 TTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGCGTCCTAACGCAAAAGCTGG 4344

Qy       4201 GACCTTGGCGTCGGCCGGTGGCCTACCTGTCTAAAAAGCTAGACCCAGTGGCAGCTGGCT 4260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4345 GACCTTGGCGTCGGCCGGTGGCCTACCTGTCTAAAAAGCTAGACCCAGTGGCAGCTGGCT 4404

Qy       4261 GGCCCCCCTGCCTACGGATGGTGGCAGCCATTGCAGTTCTGACAAAAGATGCTGGCAAGC 4320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4405 GGCCCCCCTGCCTACGGATGGTGGCAGCCATTGCAGTTCTGACAAAAGATGCTGGCAAGC 4464

Qy       4321 TCACTATGGGACAGCCGTTGGTCATTCTGGCCCCCCATGCCGTAGAGGCACTAGTTAAGC 4380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4465 TCACTATGGGACAGCCGTTGGTCATTCTGGCCCCCCATGCCGTAGAGGCACTAGTTAAGC 4524

Qy       4381 AACCCCCTGATCGCTGGCTCTCCAATGCCCGGATGACCCATTACCAAGCCCTGCTCCTGG 4440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4525 AACCCCCTGATCGCTGGCTCTCCAATGCCCGGATGACCCATTACCAAGCCCTGCTCCTGG 4584

Qy       4441 ACACGGACCGGGTCCAGTTCGGGCCAGTAGTGGCCCTAAATCCAGCTACGCTGCTCCCTC 4500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4585 ACACGGACCGGGTCCAGTTCGGGCCAGTAGTGGCCCTAAATCCAGCTACGCTGCTCCCTC 4644

Qy       4501 TGCCTGAGGAGGGGCTGCAACATGACTGCCTTGACATCTTGGCTGAAGCCCACGGAACTA 4560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4645 TGCCTGAGGAGGGGCTGCAACATGACTGCCTTGACATCTTGGCTGAAGCCCACGGAACTA 4704

Qy       4561 GATCAGATCTTACGGACCAGCCCCTCCCAGACGCCGACCACACCTGGTACACGGATGGGA 4620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4705 GATCAGATCTTACGGACCAGCCCCTCCCAGACGCCGACCACACCTGGTACACGGATGGGA 4764

Qy       4621 GCAGCTTCCTGCAAGAAGGGCAGCGTAAGGCCGGAGCAGCGGTGACCACTGAGACTGAGG 4680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4765 GCAGCTTCCTGCAAGAAGGGCAGCGTAAGGCCGGAGCAGCGGTGACCACTGAGACTGAGG 4824

Qy       4681 TAATCTGGGCCAGGGCATTGCCAGCCGGGACATCGGCCCAAAGAGCTGAACTGATAGCGC 4740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4825 TAATCTGGGCCAGGGCATTGCCAGCCGGGACATCGGCCCAAAGAGCTGAACTGATAGCGC 4884

Qy       4741 TCACCCAAGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTT 4800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4885 TCACCCAAGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTT 4944

Qy       4801 ACGCTTTTGCCACCGCCCATATTCATGGAGAAATATACAGAAGGCGCGGGTTGCTCACAT 4860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4945 ACGCTTTTGCCACCGCCCATATTCATGGAGAAATATACAGAAGGCGCGGGTTGCTCACAT 5004

Qy       4861 CAGAAGGAAAAGAGATCAAGAACAAGGACGAGATCTTAGCCCTACTAAAGGCTCTCTTCT 4920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5005 CAGAAGGAAAAGAGATCAAGAACAAGGACGAGATCTTAGCCCTACTAAAGGCTCTCTTCT 5064

Qy       4921 TGCCCAAAAGACTTAGCATAATTCATTGCCCGGGACATCAAAAAGGAAACAGCGCAGAGG 4980
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5065 TGCCCAAAAGACTTAGCATAATTCATTGCCCGGGACATCAAAAAGGAAACAGCGCAGAGG 5124

Qy        4981 CCAGGGGCAACCGGATGGCCGACCAAGCGGCCCGAGAAGTAGCCACTAGAGAAACTCCAG 5040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5125 CCAGGGGCAACCGGATGGCCGACCAAGCGGCCCGAGAAGTAGCCACTAGAGAAACTCCAG 5184

Qy        5041 GAACTTCCACACTTCTGATAGAAAACTCAACCCCCTATACCCATGAACACTTTCACTATA 5100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5185 GAACTTCCACACTTCTGATAGAAAACTCAACCCCCTATACCCATGAACACTTTCACTATA 5244

Qy        5101 CAGTAACTGACACAAAGGATTTGACCAAACTAGGAGCCACTTATGACAGTGCGAAGAAAT 5160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5245 CAGTAACTGACACAAAGGATTTGACCAAACTAGGAGCCACTTATGACAGTGCGAAGAAAT 5304

Qy        5161 ATTGGGTCTATCAAGGAAAGCCTGTTATGCCTGATCAATTCACCTTTGAGTTACTAGACT 5220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5305 ATTGGGTCTATCAAGGAAAGCCTGTTATGCCTGATCAATTCACCTTTGAGTTACTAGACT 5364

Qy        5221 TTCTTCACCAATTGACCCACCTCAGCTTCTCAAAAACAAAGGCTCTCCTAGAGAGAAGCC 5280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5365 TTCTTCACCAATTGACCCACCTCAGCTTCTCAAAAACAAAGGCTCTCCTAGAGAGAAGCC 5424

Qy        5281 CCAGTCCCTACTACATGCTGAACCGGGATCGAACACTCAAAAATATCACTGAGACCTGCA 5340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5425 CCAGTCCCTACTACATGCTGAACCGGGATCGAACACTCAAAAATATCACTGAGACCTGCA 5484

Qy        5341 AAGCTTGTGCACAAGTCAATGCCAGCAAGTCTGCCGTTAAGCAAGGAACTAGGGTCCGCG 5400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5485 AAGCTTGTGCACAAGTCAATGCCAGCAAGTCTGCCGTTAAGCAAGGAACTAGGGTCCGCG 5544

Qy        5401 GGCATCGGCCTGGCACACACTGGGAGATCGATTTCACCGAGGTAAAACCTGGATTGTATG 5460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5545 GGCATCGGCCTGGCACACACTGGGAGATCGATTTCACCGAGGTAAAACCTGGATTGTATG 5604

Qy        5461 GCTATAAGTATCTTTTAGTTTTTGTAGATACTTTTTCTGGCTGGATAGAAGCTTTCCCAA 5520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5605 GCTATAAGTATCTTTTAGTTTTTGTAGATACTTTTTCTGGCTGGATAGAAGCTTTCCCAA 5664

Qy        5521 CTAAGAAAGAAACCGCCAAGGTCGTGACCAAGAAACTGCTAGAAGAGATCTTCCCTAGGT 5580
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5665 CTAAGAAAGAAACCGCCAAGGTCGTGACCAAGAAACTGCTAGAAGAGATCTTCCCTAGGT 5724

Qy        5581 TCGGCATGCCGCAGGTATTGGGAACTGACAATGGGCCTGCCTTCGTCTCCAAGGTGAGTC 5640
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5725 TCGGCATGCCGCAGGTATTGGGAACTGACAATGGGCCTGCCTTCGTCTCCAAGGTGAGTC 5784

Qy        5641 AGACAGTGGCCGATCTGTTGGGGATTGATTGGAAATTACATTGTGCATACAGACCCCAAA 5700
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5785 AGACAGTGGCCGATCTGTTGGGGATTGATTGGAAATTACATTGTGCATACAGACCCCAAA 5844

Qy        5701 GCTCAGGTCAGGTAGAAAGAATGAATAGGACCATCAAGGAGACTTTAACTAAATTAACGC 5760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5845 GCTCAGGTCAGGTAGAAAGAATGAATAGGACCATCAAGGAGACTTTAACTAAATTAACGC 5904

Qy        5761 TTGCAACTGGCTCTAGAGACTGGGTGCTCCTACTCCCCTTAGCCCTGTACCGAGCCCGCA 5820
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5905 TTGCAACTGGCTCTAGAGACTGGGTGCTCCTACTCCCCTTAGCCCTGTACCGAGCCCGCA 5964

Qy        5821 ACACGCCGGGCCCCCATGGCCTCACCCCATATGAGATCTTATATGGGGCACCCCCGCCCC 5880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5965 ACACGCCGGGCCCCCATGGCCTCACCCCATATGAGATCTTATATGGGGCACCCCCGCCCC 6024

Qy        5881 TTGTAAACTTCCCTGACCCTGACATGACCAGAGTTACTAACAGCCCCTCTCTCCAAGCTC 5940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6025 TTGTAAACTTCCCTGACCCTGACATGACCAGAGTTACTAACAGCCCCTCTCTCCAAGCTC 6084
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Qy          5941 ACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTTTGGAGACCACTGGCGGCAGCTTACC 6000
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6085 ACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTTTGGAGACCACTGGCGGCAGCTTACC 6144

Qy          6001 AAGAACAACTGGACCGGCCGGTGGTGCCTCACCCTTACCGGGTCGGCGACACAGTGTGGG 6060
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6145 AAGAACAACTGGACCGGCCGGTGGTGCCTCACCCTTACCGGGTCGGCGACACAGTGTGGG 6204

Qy          6061 TCCGCCGACATCAAACCAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGC 6120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6205 TCCGCCGACATCAAACCAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGC 6264

Qy          6121 TGACCACCCCCACCGCCCTCAAAGTAGACGGTATCGCAGCTTGGATACACGCAGCCCACG 6180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6265 TGACCACCCCCACCGCCCTCAAAGTAGACGGTATCGCAGCTTGGATACACGCAGCCCACG 6324

Qy          6181 TAAAGGCGGCCGACACCGAGAGTGGACCATCCTCTGGACGGACATGGCGCGTTCAACGCT 6240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6325 TAAAGGCGGCCGACACCGAGAGTGGACCATCCTCTGGACGGACATGGCGCGTTCAACGCT 6384

Qy          6241 CTCAAAACCCCCTCAAGATAAGATTAACCCGTGGAAGCCCTTAATAGTCATGGAGTCCT 6300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6385 CTCAAAACCCCCTCAAGATAAGATTAACCCGTGGAAGCCCTTAATAGTCATGGAGTCCT 6444

Qy          6301 GTTAGGAGTAGGGATGACGAGTCTGCAAAATAAGAACCCCCACCAGCCCATGACCCTCAC 6360
                 |||||||||||||||| |              ||| |||||| |||  | | |   | ||
Db          6445 GTTAGGAGTAGGGATGGC------------AGAGAGCCCCCATCAGGTCTTTAATGTAAC 6492

Qy          6361 TTGGCAGGTACTGTCCCAAACTGGAGACGTTGTCTGGGATACAAAGGCAGTCCAGCCCCC 6420
                  |||   ||      ||  |     |    |  |    || | |   |  ||| |    |
Db          6493 CTGGAGAGTCACCAACCTGATGACTGGGCGTACCGCCAATGCCACCTCCCTCCTGGGAAC 6552

Qy          6421 T---TGGACTTGGTGGCCCACACTTAAACCTGATGTATGTGCCTTGGCGGCTAGTCTTGA 6477
                 |        |   |  || | | |  |   |||| ||||||   |||  |
Db          6553 TGTACAAGATGCCTTCCCAAAATTATATTTTGATCTATGTGATCTGGTCGGAGAGGAGTG 6612

Qy          6478 GTCCTGGGATATCCCGGGAACCGATGTCTCGTCCTCTAAACGAGTCAGACCTCCGGACTC 6537
                 |  |        || || | |  |||||  |   | |    |       ||  | |
Db          6613 GGACCCTTCAGACCAGGAACCGTATGTCGGG---TATGGCTGCAAGTACCCCGCAGGGAG 6669

Qy          6538 AGACTATACTGCCGCTTATAAGCAAATCACCTGGGGAGCCATAGGGTGCAGCTACCCTCG 6597
                 | |    ||     ||| | |      |   ||    |           |  |      |
Db          6670 ACAGCGGACCCGGACTTTTGACTTTTACGTGTGCCCTGGGCATACCGTAAAGTCGGGGTG 6729

Qy          6598 GGCTAGGACTAGAATGGCAAGCTCTACCTTCTACGTATGTCCCCGGGATGGCCGGACCCT 6657
                  |   |  |  ||  ||    || |      |  |  |||         || | | |
Db          6730 TGGGGGACCAGGAGAGGGCTACTGTGGTAAATGGGGGTGTGAAACCACCGGACAGGCTTA 6789

Qy          6658 TTCAGAAGCTAGAAGGTGCGGGGGGCTAGAATCCCTATACTGTAAAGAATGGGATTGTGA 6717
                  |   |  | | |   |   |||  |||   |||||  |  |     |       || ||
Db          6790 CTGGAAGCCCACATCATCGTGGGACCTAATCTCCCTTAAGCGCGGTAACACCCCCTGGGA 6849

Qy          6718 GACCACGGGGACCGGTTATTGGCTATCTAAATCCTCAAAAGACCTCATAACTGTAAAATG 6777
                    ||||||   |  | |       | |    |||   | ||||||   |  |||
Db          6850 ---CACGGGATGCTCTAAAGTTGCCTGTGGCCCCTGCTACGACCTCTCCAAAGTA----- 6901

Qy          6778 GGACCAAAATAGCGAATGGACTCAAAAATTTCAACAGTGTCACCAGACCGGCTGGTGTAA 6837
                                     |  |    || |||  |  |   |     ||| | || ||
Db          6902 -------------------TCCAATTCCTTCCAAGGGGCTACTCGAGGGGGCAGATGCAA 6942

Qy          6838 CCCCCTTAAAATAGATTTCACAGACAAAGGAAAATTATCCAAGGACTGGATAACGGGAAA 6897
                 ||| ||     |||| ||||| ||   |||||||    | |   |||||     |   ||
Db          6943 CCCTCTAGTCCTAGAATTCACTGATGCAGGAAAAAAGGCTA---ACTGGGACGGGCCCAA 6999

Qy          6898 AACCTGGGGATTAAGATTCTATGTGTCTGGACATCCAGGCGTACAGTTCACCATTCGCTT 6957
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               | | |||||| | ||| | ||          |   ||||   | |    |  |     ||
Db        7000 ATCGTGGGACTGAGACTGTA---------CCGGACAGGAACAGATCCTATTACCATGTT 7050

Qy        6958 AAAAATCACCAACATGCCAGCTGTGGCAGTAGGTCCTGACCTCGTCCTTGTGGAACAAGG 7017
                    | |||     |     |   |  | |   |  | || | |        | | ||
Db        7051 CTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGTCCCCATAGGGCCCAACCCAGT 7110

Qy        7018 ACCTCCTAGAACGTCCCTCGCTCTCCCACCTCCTCTTCCCCCAAGGGAAGCGCCACCGCC 7077
               |   ||          ||| ||  | ||||            |  ||   | |  || ||
Db        7111 ATTACCCGACCAAAGACTCCCTTCCTCACCAATAGAGATTGTACCGGCTCCACAGCCACC 7170

Qy        7078 ATCTCTCCCCGACTCTAACTCCACAGCCCTGGCGACTAGTGCACAAACTCCCACGGTGAG 7137
                   | || | |  | |  | | |  |     | || ||| |||   |  || |    |
Db        7171 TAGCCCCCTCAATACCAGTTACCCCCCTTCCACTACCAGTACACCCTCAACCTCCCCTAC 7230

Qy        7138 AAAAACAATTGTTACCCTAAACACTCCGCCTCCCACCACAGGCGACAGACTTTTTGATCT 7197
               ||   ||| |||  | |        || || ||    || || || |||||  | | |||
Db        7231 AAGTCCAAGTGTCCCACAG------CCACCCCCAGGAACTGGAGATAGACTACTAGCTCT 7284

Qy        7198 TGTGCAGGGGGCCTTCCTAACCTTAAATGCTACCAACCCAGGGGCCACTGAGTCTTGCTG 7257
                ||  | || ||||  |   |  | ||    ||||| || |     ||  |    || ||
Db        7285 AGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAAGACCCAAGAATGTTG 7344

Qy        7258 GCTTTGTTTGGCCATGGGCCCCCCTTATTATGAAGCAATAGCCTCATCAGG---AGAGGT 7314
               ||| || || |    ||| || |||||||| |||| | ||||       ||     |
Db        7345 GCTGTGCTTAGTGTCGGGACCTCCTTATTACGAAGGAGTAGCGGTCGTGGGCACTTATAC 7404

Qy        7315 CGCCTACTCCACCGACCTTGACCGGTGCCGCTGGGGGACCCAAGGAAAGCTCACCCTCAC 7374
               |    | |||||||  |  | |   ||           |||||   ||||| |||||  |
Db        7405 CAATCATTCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACATAAGCTTACCCTATC 7464

Qy        7375 TGAGGTCTCAGGACACGGGTTGTGCATAGGAAAGGTGCCCTTTACCCATCAGCATCTCTG 7434
               ||| ||  ||||||| ||  | ||||| ||    || ||    || || |||    | ||
Db        7465 TGAAGTGACAGGACAGGGCCTATGCATGGGGGCAGTACCTAAAACTCACCAGGCCTTATG 7524

Qy        7435 CAATCAGACCCTATCCATCAATTCCTCCGGAGACCATCAGTATCTGCTCCCCTCCAACCA 7494
                ||    |||| |  |  |   ||      ||      | || ||     ||  |
Db        7525 TAACACCACCCAAAGCGCCGGCTC------AGGATCCTACTACCTTGCAGCACCCGCCGG 7578

Qy        7495 TAGCTGGTGGGCTTGCAGCACTGGCCTCACCCCTTGCCTCTCCACCTCAGTTTTTAATCA 7554
                |    ||||||||||||||||||  | || || ||| | |||||| | ||  | ||||
Db        7579 AACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGTGCTCAATCT 7638

Qy        7555 GACTAGAGATTTCTGTATCCAGGTCCAGCTGATTCCTCGCATCTATTACTATCCTGAAGA 7614
                || | |||||  ||| |    ||  | ||    ||  |  |   |||| |  |    ||
Db        7639 AACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCACTCCCCCGA 7698

Qy        7615 AGTTTTGTTACAGGCCTATGACAATTCTCACCCCAGGACTAAAAGAGAGGCTGTCTCACT 7674
                  | |||   | |   |     |    |   |||    |||||||||| | || ||| |
Db        7699 TTATATGT---ATGGTCAGCTTGAACAGCGTACCAAATATAAAAGAGAGCCAGTATCATT 7755

Qy        7675 TACCCTAGCTGTTTTACTGGGGTTGGAATCACGGCGGGAATAGGTACTGGTTCAACTGC 7734
                ||||| ||  || |||| ||      || || || || || | ||||   |    |
Db        7756 GACCCTGGCCCTTCTACTAGGAGGATTAACCATGGAGGGATTGCAGCTGGAATAGGGAC 7815

Qy        7735 CTTAATTAAAGGACCTATAGACCTCCAGCAAGGCCTGACAAGCCTCCAGATCGCCATAGA 7794
                   |  |  |     ||  |   ||||||     |       || ||   ||| ||  |
Db        7816 GGGGACCACTGCCTTAATTAAAACCCAGCA---GTTTGAGCAGCTTCATGCCGCTATCCA 7872

Qy        7795 TGCTGACCTCCGGGCCCTCCAAGACTCAGTCAGCAAGTTAGAGGACTCACTGACTTCCCT 7854
                 | ||||||   |   || || | ||| | | |||  ||||  | |||||||| ||  |
Db        7873 GACAGACCTCAACGAAGTCGAAAAGTCAATTACCAACCTAGAAAAGTCACTGACCTCGTT 7932

Qy        7855 GTCCGAGGTAGTGCTCCAAAATAGGAGAGGCCTTGACTTGCTGTTTCTAAAAGAAGGTGG 7914
               ||| || ||||| || || ||  | |||||||| || ||||| || ||||| || || ||
Db        7933 GTCTGAAGTAGTCCTACAGAACCGCAGAGGCCTAGATTTGCTATTCCTAAAGGAGGGAGG 7992
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Qy        7915 CCTCTGTGCGGCCCTAAAGGAAGAGTGCTGTTTTTACATAGACCACTCAGGTGCAGTACG 7974
                ||||| || |||||||| ||||| || ||||||||   ||||||| | ||   |||  |
Db        7993 TCTCTGCGCAGCCCTAAAAGAAGAATGTTGTTTTTATGCAGACCACACGGGGCTAGTGAG 8052

Qy        7975 GGACTCCATGAAAAAACTCAAAGAAAAACTGGATAAAAGACAGTTAGAGCGCCAGAAAAG 8034
                |||  ||||   ||| | | |||||  ||  || | |||||   |       ||| | |
Db        8053 AGACAGCATGGCCAAATTAAGAGAAAGGCTTAATCAGAGACAAAAACTATTTGAGACAGG 8112

Qy        8035 CCAAAACTGGTATGAAGGATGGTTCAATAACTCCCCTTGGTTCACTACCCTGCTATCAAC 8094
               ||||   ||||  |||||   ||| ||||  ||||| ||||| || ||| |  | || ||
Db        8113 CCAAGGATGGTTCGAAGGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTCCAC 8172

Qy        8095 CATCGCTGGGCCCCTATTACTCCTCCTTCTGTTGCTCATCCTCGGGCCATGCATCATCAA 8154
               ||||   || || ||| || | ||| | ||| |  |  || | || || |||||  ||||
Db        8173 CATCATGGGACCTCTAATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCATTCTCAA 8232

Qy        8155 TCGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCA 8214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8233 TCGATTAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCA 8292

Qy        8215 ACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATT 8274
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8293 ACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAATAAAAGATTTTATT 8352

Qy        8275 TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTA 8334
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8353 TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTA 8412

Qy        8335 AGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATC 8394
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8413 AGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATC 8472

Qy        8395 AAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG 8454
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8473 AAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG 8532

Qy        8455 TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGAT 8514
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8533 TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGAT 8592

Qy        8515 ATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG 8574
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8593 ATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG 8652

Qy        8575 GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT 8634
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8653 GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT 8712

Qy        8635 GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCG 8694
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8713 GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCG 8772

Qy        8695 CGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCC 8754
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8773 CGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCC 8832

Qy        8755 TCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATC 8814
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8833 TCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATC 8892

Qy        8815 CGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG 8874
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8893 CGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG 8952

Qy        8875 CGGGGGTCTTTCATT 8889
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                 |||||||||||||||
Db        8953 CGGGGGTCTTTCATT 8967
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